

Sequences

[0087] <120> PEG-conjugates of NK4

<130> Case 20859

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<150> 01104640.6

<151> 2001-02-23

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1344

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1344)

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10

15

act acc cta atc aaa ata gat cca gca ctg aag ata aaa acc aaa aaa 96

Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys

20

25

30

gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa gga			144
Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly			
35	40	45	
ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa caa			192
Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln			
50	55	60	
tgc ctc tgg ttc ccc ttc aat agc atg tca agt gga gtg aaa aaa gaa			240
Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu			
65	70	75	80
ttt ggc cat gaa ttt gac ctc tat gaa aac aaa gac tac att aga aac			288
Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn			
85	90	95	
tgc atc att ggt aaa gga cgc agc tac aag gga aca gta tct atc act			336
Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr			
100	105	110	
aag agt ggc atc aaa tgt cag ccc tgg agt tcc atg ata cca cac gaa			384
Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu			
115	120	125	
cac agc ttt ttg cct tcg agc tat cgg ggt aaa gac cta cag gaa aac			432
His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn			
130	135	140	
tac tgt cga aat cct cga ggg gaa gaa ggg gga ccc tgg tgt ttc aca			480
Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr			
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agc aat cca gag gta cgc tac gaa gtc tgt gac att cct cag tgt tca			528
Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser			
165	170	175	

gaa gtt gaa tgc atg acc tgc aat ggg gag agt tat cga ggt ctc atg 576
 Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met
 180 185 190

gat cat aca gaa tca ggc aag att tgt cag cgc tgg gat cat cag aca 624
 Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr
 195 200 205

cca cac cgg cac aaa ttc ttg cct gaa aga tat ccc gac aag ggc ttt 672
 Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
 210 215 220

gat gat aat tat tgc cgc aat ccc gat ggc cag ccg agg cca tgg tgc 720
 Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys
 225 230 235 240

tat act ctt gac cct cac acc cgc tgg gag tac tgt gca att aaa aca 768
 Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr
 245 250 255

tgc gct gac aat act atg aat gac act gat gtt cct ttg gaa aca act 816
 Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr
 260 265 270

gaa tgc atc caa ggt caa gga gaa ggc tac agg ggc act gtc aat acc 864
 Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr
 275 280 285

att tgg aat gga att cca tgt cag cgt tgg gat tct cag tat cct cac 912
 Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His
 290 295 300

gag cat gac atg act cct gaa aat ttc aag tgc aag gac cta cga gaa 960
 Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu
 305 310 315 320

aat tac tgc cga aat cca gat ggg tct gaa tca ccc tgg tgt ttt acc 1008
Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr
325 330 335

act gat cca aac atc cga gtt ggc tac tgc tcc caa att cca aac tgt 1056
Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys
340 345 350

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Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr
355 360 365

atg ggc aac tta tcc caa aca aga tct gga cta aca tgt tca atg tgg 1152
Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp
370 375 380

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Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
385 390 395 400

gca agt aag ctg aat gag aat tac tgc cga aat cca gat gat gat gct 1248
Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala
405 410 415

cat gga ccc tgg tgc tac acg gga aat cca ctc att cct tgg gat tat 1296
His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
420 425 430

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Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
35 40 45

Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
50 55 60

Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
65 70 75 80

Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
85 90 95

Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
100 105 110

Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
115 120 125

His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn
130 135 140

Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr
145 150 155 160

Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser
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Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met
180 185 190

Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr
195 200 205

Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
210 215 220

Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys
225 230 235 240
Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr
245 250 255
Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr
260 265 270

Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr
275 280 285
Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His
290 295 300
Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu
305 310 315 320
Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr
325 330 335
Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys
340 345 350
Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr
355 360 365
Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp
370 375 380
Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
385 390 395 400
Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala
405 410 415
His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
420 425 430
Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
435 440 445